

## SEQUENCE LISTING

<110> C. Frank Bennett  
Susan M. Freier

<120> ANTISENSE MODULATION OF NAC EXPRESSION

<130> RTS-0326

<160> 91

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<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

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<212> DNA

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<223> Antisense Oligonucleotide

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;222&gt; (523) ... (4812)

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cggcgtctat ctgttaggtgc cctgggattt ataaaactgg gttccgaatg ctgaataaga 420

gacggtaaga gccaaggcaa aggacagcac tggtctctgc ctgcctgata ccctcaccac 480

ctgggaacat ccccgagaca ccctcttaac tccgggacag ag atg gct ggc gga 534  
Met Ala Gly Gly

1

gcc tgg ggc cgc ctg gcc tgt tac ttg gag ttc ctg aag aag gag gag 582  
Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu Lys Lys Glu Glu

5

10

15

20

ctg aag gag ttc cag ctt ctg ctc gcc aat aaa gcg cac tcc agg agc 630  
Leu Lys Glu Phe Gln Leu Leu Ala Asn Lys Ala His Ser Arg Ser  
25 30 35tct tcg ggt gag aca ccc gct cag cca gag aag acg agt ggc atg gag 678  
Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr Ser Gly Met Glu  
40 45 50gtg gcc tcg tac ctg gtg gct cag tat ggg gag cag cgg gcc tgg gac 726  
Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln Arg Ala Trp Asp

55	60	65	
cta gcc ctc cat acc tgg gag cag atg ggg ctg agg tca ctg tgc gcc			774
Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg Ser Leu Cys Ala			
70	75	80	
- - - caa gcc cag gaa ggg gca ggc cac tct ccc tca ttc ccc tac agc cca			822
Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe Pro Tyr Ser Pro			
85	90	95	100
agt gaa ccc cac ctg ggg tct ccc agc caa ccc acc tcc acc gca gtg			870
Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr Ser Thr Ala Val			
105	110	115	
cta atg ccc tgg atc cat gaa ttg ccg gcg ggg tgc acc cag ggc tca			918
Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys Thr Gln Gly Ser			
120	125	130	
gag aga agg gtt ttg aga cag ctg cct gac aca tct gga cgc cgc tgg			966
Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser Gly Arg Arg Trp			
135	140	145	
aga gaa atc tct gcc tca ctc ctc tac caa gct ctt cca agc tcc cca			1014
Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu Pro Ser Ser Pro			
150	155	160	
gac cat gag tct cca agc cag gag tca ccc aac gcc ccc aca tcc aca			1062
Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala Pro Thr Ser Thr			
165	170	175	180
gca gtg ctg ggg agc tgg gga tcc cca cct cag ccc agc cta gca ccc			1110
Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro Ser Leu Ala Pro			
185	190	195	
aga gag cag gag gct cct ggg acc caa tgg cct ctg gat gaa acg tca			1158
Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu Asp Glu Thr Ser			
200	205	210	
gga att tac tac aca gaa atc aga gaa aga gag aga gag aaa tca gag			1206
Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg Lys Ser Glu			
215	220	225	
aaa ggc agg ccc cca tgg gca gcg gtg gtá gga acg ccc cca cag gcg			1254
Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr Pro Pro Gln Ala			

230	235	240	
cac acc agc cta cag ccc cac cac ccc cca tgg gag cct tct gtg aga			1302
His Thr Ser Leu Gln Pro His His Pro Trp Glu Pro Ser Val Arg			
245	250	255	260
---gag agc ctc tgt tcc aca tgg ccc tgg aaa aat gag gat ttt aac caa			1350
Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu Asp Phe Asn Gln			
265	270	275	
aaa ttc aca cag ctg cta ctt cta caa aga cct cac ccc aga agc caa			1398
Lys Phe Thr Gln Leu Leu Leu Gln Arg Pro His Pro Arg Ser Gln			
280	285	290	
gat ccc ctg gtc aag aga agc tgg cct gat tat gtg gag gag aat cga			1446
Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val Glu Glu Asn Arg			
295	300	305	
gga cat tta att gag atc aga gac tta ttt ggc cca ggc ctg gat acc			1494
Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro Gly Leu Asp Thr			
310	315	320	
caa gaa cct cgc ata gtc ata ctg cag ggg gct gct gga att ggg aag			1542
Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala Gly Ile Gly Lys			
325	330	335	340
tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg aga ggc cag ctg			1590
Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly Arg Gly Gln Leu			
345	350	355	
tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc tgc aga gag ctg			1638
Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser Cys Arg Glu Leu			
360	365	370	
gcc cag tcc aag gtg gtg agt ctc gct gag ctc atc gga aaa gat ggg			1686
Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile Gly Lys Asp Gly			
375	380	385	
aca gcc act ccg gct ccc att aga cag atc ctg tct agg cca gag cgg			1734
Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser Arg Pro Glu Arg			
390	395	400	
ctg ctc ttc atc ctc gat ggt gta gat gag cca gga tgg gtc ttg cag			1782
Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly Trp Val Leu Gln			

405	410	415	420	
gag ccg agt tct gag ctc tgt ctg cac tgg agc cag cca cag ccg gcg				1830
Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln Pro Gln Pro Ala				
425	430	435		
- - - gat gca ctg ctg ggc agt ttg ctg ggg aaa act ata ctt ccc gag gca				1878
Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile Leu Pro Glu Ala				
440	445	450		
tcc ttc ctg atc acg gct cgg acc aca gct ctg cag aac ctc att cct				1926
Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln Asn Leu Ile Pro				
455	460	465		
tct ttg gag cag gca cgt tgg gta gag gtc ctg ggg ttc tct gag tcc				1974
Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly Phe Ser Glu Ser				
470	475	480		
agc agg aag gaa tat ttc tac aga tat ttc aca gat gaa agg caa gca				2022
Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp Glu Arg Gln Ala				
485	490	495	500	
att aga gcc ttt agg ttg gtc aaa tca aac aaa gag ctc tgg gcc ctg				2070
Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu Leu Trp Ala Leu				
505	510	515		
tgt ctt gtg ccc tgg gtg tcc tgg ctg gcc tgc act tgc ctg atg cag				2118
Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr Cys Leu Met Gln				
520	525	530		
cag atg aag cgg aag gaa aaa ctc aca ctg act tcc aag acc acc aca				2166
Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser Lys Thr Thr Thr				
535	540	545		
acc ctc tgt cta cat tac ctt gcc cag gct ctc caa gct cag cca ttg				2214
Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln Ala Gln Pro Leu				
550	555	560		
gga ccc cag ctc aga gac ctc tgc tct ctg gct gct gag ggc atc tgg				2262
Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala Glu Gly Ile Trp				
565	570	575	580	
caa aaa aag acc ctt ttc agt cca gat gac ctc agg aag cat ggg tta				2310
Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg Lys His Gly Leu				

585	590	595	
gat ggg gcc atc atc tcc acc ttc ttg aag atg ggt att ctt caa gag			2358
Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly Ile Leu Gln Glu			
600	605	610	
—cac ccc atc cct ctg agc tac agc ttc att cac ctc tgt ttc caa gag			2406
His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu Cys Phe Gln Glu			
615	620	625	
ttc ttt gca gca atg tcc tat gtc ttg gag gat gag aag ggg aga ggt			2454
Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu Lys Gly Arg Gly			
630	635	640	
aaa cat tct aat tgc atc ata gat ttg gaa aag acg cta gaa gca tat			2502
Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr Leu Glu Ala Tyr			
645	650	655	660
gga ata cat ggc ctg ttt ggg gca tca acc aca cgt ttc cta ttg ggc			2550
Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg Phe Leu Leu Gly			
665	670	675	
ctg tta agt gat gag ggg gag aga gag atg gag aac atc ttt cac tgc			2598
Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn Ile Phe His Cys			
680	685	690	
cg <sup>g</sup> ctg tct cag ggg agg aac ctg atg cag tgg gtc ccg tcc ctg cag			2646
Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val Pro Ser Leu Gln			
695	700	705	
ctg ctg ctg cag cca cac tct ctg gag tcc ctc cac tgc ttg tac gag			2694
Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His Cys Leu Tyr Glu			
710	715	720	
act cg <sup>g</sup> aac aaa acg ttc ctg aca caa gtg atg gcc cat ttc gaa gaa			2742
Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala His Phe Glu Glu			
725	730	735	740
atg ggc atg tgt gta gaa aca gac atg gag ctc tta gtg tgc act ttc			2790
Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu Val Cys Thr Phe			
745	750	755	
tgc att aaa ttc agc cgc cac gtg aag aag ctt cag ctg att gag ggc			2838
Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln Leu Glu Gly			

760	765	770	
agg cag cac aga tca aca tgg agc ccc acc atg gta gtc ctg ttc agg Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val Val Leu Phe Arg			2886
775	780	785	
— tgg gtc cca gtc aca gat gcc tat tgg cag att ctc ttc tcc gtc ctc Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu Phe Ser Val Leu			2934
790	795	800	
aag gtc acc aga aac ctg aag gag ctg gac cta agt gga aac tcg ctg Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser Gly Asn Ser Leu			2982
805	810	815	820
agc cac tct gca gtg aag agt ctt tgt aag acc ctg aga cgc cct cgc Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu Arg Arg Pro Arg			3030
825	830	835	
tgc ctc ctg gag acc ctg cgg ttg gct ggc tgt ggc ctc aca gct gag Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly Leu Thr Ala Glu			3078
840	845	850	
gac tgc aag gac ctt gcc ttt ggg ctg aga gcc aac cag acc ctg acc Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn Gln Thr Leu Thr			3126
855	860	865	
gag ctg gac ctg agc ttc aat gtg ctc acg gat gct gga gcc aaa cac Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala Gly Ala Lys His			3174
870	875	880	
ctt tgc cag aga ctg aga cag ccg agc tgc aag cta cag cga ctg cag Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu Gln Arg Leu Gln			3222
885	890	895	900
ctg gtc agc tgt ggc ctc acg tct gac tgc tgc cag gac ctg gcc tct Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln Asp Leu Ala Ser			3270
905	910	915	
gtg ctt agt gcc agc ccc agc ctg aag gag cta gac ctg cag cag aac Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp Leu Gln Gln Asn			3318
920	925	930	
aac ctg gat gac gtt ggc gtg cga ctg ctc tgt gag ggg ctc agg cat Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu Gly Leu Arg His			3366

935

940

945

cct gcc tgc aaa ctc ata cgc ctg ggg ctg gac cag aca act ctg agt 3414  
Pro Ala Cys Lys Leu Ile Arg Leu Gly Leu Asp Gln Thr Thr Leu Ser  
950 955 960

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Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln Glu Lys Pro Gln  
965 970 975 980

ctg ctc atc ttc agc aga cgg aaa cca agt gtg atg acc cct act gag 3510  
Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met Thr Pro Thr Glu  
985 990 995

ggc ctg gat acg gga gag atg agt aat agc aca tcc tca ctc aag cgg 3558  
Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser Ser Leu Lys Arg  
1000 1005 1010

cag aga ctc gga tca gag agg gcg gct tcc cat gtt gct cag gct aat 3606  
Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His Val Ala Gln Ala Asn  
1015 1020 1025

ctc aaa ctc ctg gac gtg agc aag atc ttc cca att gct gag att gca 3654  
Leu Lys Leu Leu Asp Val Ser Lys Ile Phe Pro Ile Ala Glu Ile Ala  
1030 1035 1040

gag gaa agc tcc cca gag gta gta ccg gtg gaa ctc ttg tgc gtg cct 3702  
Glu Glu Ser Ser Pro Glu Val Val Pro Val Glu Leu Leu Cys Val Pro  
1045 1050 1055 1060

tct cct gcc tct caa ggg gac ctg cat acg aag cct ttg ggg act gac 3750  
Ser Pro Ala Ser Gln Gly Asp Leu His Thr Lys Pro Leu Gly Thr Asp  
1065 1070 1075

gat gac ttc tgg ggc ccc acg ggg cct gtg gct act gag gta gtt gac 3798  
Asp Asp Phe Trp Gly Pro Thr Gly Pro Val Ala Thr Glu Val Val Asp  
1080 1085 1090

aaa gaa aag aac ttg tac cga gtt cac ttc cct gta gct ggc tcc tac 3846  
Lys Glu Lys Asn Leu Tyr Arg Val His Phe Pro Val Ala Gly Ser Tyr  
1095 1100 1105

cgc tgg ccc aac acg ggt ctc tgc ttt gtg atg aga gaa gcg gtg acc 3894  
Arg Trp Pro Asn Thr Gly Leu Cys Phe Val Met Arg Glu Ala Val Thr

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gtt gag att gaa ttc tgt gtg tgg gac cag ttc ctg ggt gag atc aac Val Glu Ile Glu Phe Cys Val Trp Asp Gln Phe Leu Gly Glu Ile Asn			3942
1125	1130	1135	1140
— cca cag cac agc tgg atg gtg gca ggg cct ctg ctg gac atc aag gct Pro Gln His Ser Trp Met Val Ala Gly Pro Leu Leu Asp Ile Lys Ala			3990
1145	1150	1155	
gag cct gga gct gtg gaa gct gtg cac ctc cct cac ttt gtg gct ctc Glu Pro Gly Ala Val Glu Ala Val His Leu Pro His Phe Val Ala Leu			4038
1160	1165	1170	
caa ggg ggc cat gtg gac aca tcc ctg ttc caa atg gcc cac ttt aaa Gln Gly His Val Asp Thr Ser Leu Phe Gln Met Ala His Phe Lys			4086
1175	1180	1185	
gag gag ggg atg ctc ctg gag aag cca gcc agg gtg gag ctg cat cac Glu Glu Gly Met Leu Leu Glu Lys Pro Ala Arg Val Glu Leu His His			4134
1190	1195	1200	
ata gtt ctg gaa aac ccc agc ttc tcc ccc ttg gga gtc ctc ctg aaa Ile Val Leu Glu Asn Pro Ser Phe Ser Pro Leu Gly Val Leu Leu Lys			4182
1205	1210	1215	1220
atg atc cat aat gcc ctg cgc ttc att ccc gtc acc tct gtg gtg ttg Met Ile His Asn Ala Leu Arg Phe Ile Pro Val Thr Ser Val Val Leu			4230
1225	1230	1235	
ctt tac cac cgc gtc cat cct gag gaa gtc acc ttc cac ctc tac ctg Leu Tyr His Arg Val His Pro Glu Glu Val Thr Phe His Leu Tyr Leu			4278
1240	1245	1250	
atc cca agt gac tgc tcc att cgg aag gaa ctg gag ctc tgc tat cga Ile Pro Ser Asp Cys Ser Ile Arg Lys Glu Leu Glu Leu Cys Tyr Arg			4326
1255	1260	1265	
agc cct gga gaa gac cag ctg ttc tcg gag ttc tac gtt ggc cac ttg Ser Pro Gly Glu Asp Gln Leu Phe Ser Glu Phe Tyr Val Gly His Leu			4374
1270	1275	1280	
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Val Trp Glu Ala Leu Val Lys Pro Gly Asp Leu Met Pro Ala Thr Thr				
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Leu Ile Pro Pro Ala Arg Ile Ala Val Pro Ser Pro Leu Asp Ala Pro				
1320		1325		1330
cag ttg ctg cac ttt gtg gac cag tat cga gag cag ctg ata gcc cga				4566
Gln Leu Leu His Phe Val Asp Gln Tyr Arg Glu Gln Leu Ile Ala Arg				
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gtg aca tcg gtg gag gtc ttg gac aaa ctg cat gga cag gtg ctg				4614
Val Thr Ser Val Glu Val Val Leu Asp Lys Leu His Gly Gln Val Leu				
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agc cag gag cag tac gag agg gtg ctg gct gag aac acg agg ccc agc				4662
Ser Gln Glu Gln Tyr Glu Arg Val Leu Ala Glu Asn Thr Arg Pro Ser				
1365		1370		1380
cag atg cgg aag ctg ttc agc ttg agc cag tcc tgg gac cgg aag tgc				4710
Gln Met Arg Lys Leu Phe Ser Leu Ser Gln Ser Trp Asp Arg Lys Cys				
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aaa gat gga ctc tac caa gcc ctg aag gag acc cat cct cac ctc att				4758
Lys Asp Gly Leu Tyr Gln Ala Leu Lys Glu Thr His Pro His Leu Ile				
1400		1405		1410
atg gaa ctc tgg gag aag ggc agc aaa aag gga ctc ctg cca ctc agc				4806
Met Glu Leu Trp Glu Lys Gly Ser Lys Lys Gly Leu Leu Pro Leu Ser				
1415		1420		1425
agc tga agtatcaaca ccagcccttg acccttgagt cctggctttg gctgaccctt				4862
Ser				
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- ggctttgtac aggaagatct acaagagcaa gccaacagag taaagtggaa ggaagttat 5282  
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23

<210> 5  
<211> 22  
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<400> 5  
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22

<210> 6  
<211> 33  
<212> DNA

<213> Artificial Sequence

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<223> PCR Probe

- - - <400> 6

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33

<210> 7

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> PCR Primer

<400> 7

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<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 8

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20

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Probe

&lt;400&gt; 9

caagcttccc gttctcagcc

20

&lt;210&gt; 10

&lt;211&gt; 96649

- - - &lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(96649)

&lt;223&gt; n = A,T,C or G

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taagatacac ttgtgtacga agttggttat caccatgtgg ctggtaacag gaaaatgcaa 180  
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actatgaaaaa actcaacaat tacaaaaaga gaagaaaagaa cgacttagat ccatatgtac 300  
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Leu Leu His Phe Val Asp Gln Tyr Arg Glu Gln Leu Ile Ala Arg Val  
1335 1340 1345

aca tcg gtg gag gtt gtc ttg gac aaa ctg cat gga cag gtg ctg agc 4254  
Thr Ser Val Glu Val Val Leu Asp Lys Leu His Gly Gln Val Leu Ser  
1350 1355 1360 1365

cag gag cag tac gag agg gtg ctg gct gag aac acg agg ccc agc cag 4302  
Gln Glu Gln Tyr Glu Arg Val Leu Ala Glu Asn Thr Arg Pro Ser Gln  
1370 1375 1380

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Met Arg Lys Leu Phe Ser Leu Ser Gln Ser Trp Asp Arg Lys Cys Lys  
1385 1390 1395

gat gga ctc tac caa gcc ctg aag gag acc cat cct cac ctc att atg 4398  
Asp Gly Leu Tyr Gln Ala Leu Lys Glu Thr His Pro His Leu Ile Met  
1400 1405 1410

gaa ctc tgg gag aag ggc agc aaa aag gga ctc ctg cca ctc agc agc 4446  
Glu Leu Trp Glu Lys Gly Ser Lys Lys Gly Leu Leu Pro Leu Ser Ser  
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ccttgggtct cagtttcttt ctctgcaaac aagttgccat ctggttgcc ttccagcact 4559

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acctgatccc aagtgactgc tccattcgg aggccataga tgatctagaa atgaaattcc 180  
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aaccaggaga tctcatgcct gcaactactc tgatccctcc agcccgata ggaaggaaca 480  
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cctgcggcag taccaatgaa gccagagagg gcttggtgga tgacaaggag gcctgagtag 600  
accgcaggtg ggtctgagaa atgggcttag gtgaggcagg tcttgaagg atttgttctt 660  
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&lt;210&gt; 48

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;223&gt; Antisense Oligonucleotide

&lt;400&gt; 48

caaagtgagg gaggtgcaca

20

&lt;210&gt; 49

&lt;211&gt; 20

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

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&lt;210&gt; 89

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Antisense Oligonucleotide

&lt;400&gt; 89

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&lt;210&gt; 90

&lt;211&gt; 20

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Antisense Oligonucleotide

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